

1

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Kindsvogel, Wayne
Gross, Jane A.
Sheppard, Paul

(A) ADDRESSEE: Townsend and Townsend and Crew LLP
(B) STREET: Two Embarcadero Center, Eighth Floor
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94111-3834

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(A) APPLICATION NUMBER: US 09/261,811
(B) FILING DATE: 03-MAR-1999
(C) CLASSIFICATION:

(A) APPLICATION NUMBER: US 08/480,002
(B) FILING DATE: 07-JUN-1995

(A) APPLICATION NUMBER: US 08/482,133
(B) FILING DATE: 07-JUN-1995

(A) APPLICATION NUMBER: US 08/483,241
(B) FILING DATE: 07-JUN-1995

(A) APPLICATION NUMBER: US 60/005,964
(B) FILING DATE: 27-OCT-1995

(A) APPLICATION NUMBER: US 08/657,581
(B) FILING DATE: 07-JUN-1996

(A) NAME: Parent, Annette S.
(B) REGISTRATION NUMBER: 42,058
(C) REFERENCE/DOCKET NUMBER: 014058-005630US

(A) TELEPHONE: (415) 576-0200
(B) TELEFAX: (415) 576-0300

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCGCAAGCTT GAATTCGAGC TCATGGTGTG TCT

33

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AATTCGATAT CATGGTGTGT CTGAAGCTCC CTGGAGGCTC CTGCATGACA GCGCTGAC

58

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CACTGTCAGC GCTGTCATGC AGGAGCCTCC AGGGAGCTTC AGACACACCA TGATATCG

58

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ACTTCTTTAA AACACATCGTG ACTCCGCGTA CACCCCCGCC ATCGGGAGGC GGGTCAGGTG 60

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATCCACCTG ACCCGCCTCC CGATGGCGGG GGTGTACGCG GAGTCACGAT GTTTTAAAG 60

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGTGACACTG ATGGTGCTGA GCTCCCCACT GGCTTTGTCT GACGAAAACC CAGTAGTGC 59

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGTGCACTA CTGGGTTTTC GTCAGACAAA GCCAGTGGGG AGCTCAGCAC CATCAGTGT 59

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

- GCCGGCTGAT GCTCCCCGCT GCACTGT

27

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCGCTCTAGA TCATATAGTT GGAGC

25

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCAGGGTCTA GATCATAAAG GCCCTGGGTG . TCTGGAG

37

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGAGGAATTC GCAGAGACCT CCCAGAGACC AGGATCC

37

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AACACTCTAG ATCACTGCAG GAGCCCTGCT GGAGGGAG

37

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGAGGAATTC TGAGTCCTGG TGACTGCCAT TACCTGT

37

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGAGCATCAG CCGGCATCAA AGAAGAACAT

30

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

| | |
|--|-----|
| GAGGATGATT AAATGAGTCG CCTCTCGAAG GTGGCTCCAG TGATTAAGC CAGAATGATG | 60 |
| GAGTATGGAA CCACAGGAGG TGGAGGCTCT GGAGGTGGAG GCTCAGGAGG A | 111 |

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

| | |
|--|----|
| GGAGGCTCAG GAGGAGGTGG GTCCGGAGAC TCCGAAAGG | 39 |
|--|----|

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

| | |
|--------------------------------------|----|
| CGCGGGATCC GATCGTGGAG GATGATTAAGA TG | 32 |
|--------------------------------------|----|

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

| | |
|----------------------------------|----|
| GCCACCTGAT CCACCCCGCA GGGAGGTGGG | 30 |
|----------------------------------|----|

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGTGGATCAG GTGGCGAAGA CGACATTGAG

30

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCGGAATTCT TAACTAGTAG CTGGGGTGAA

30

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCGGAATTCT TAACTAGTAG CTGGGGTGGA

30

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCCACCTGAT CCACCCCGCA GGGAGGTGTG

30

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CGCGGGATCC GATCGTGGAG GATGATTAAA TGTCTTTAA AAACATCGTG ACTCCGCGTA

60

CACCCCCGCC AGGAGGTGGA GGCTCTGGAG GTGGAGGCTC AGGAGGA

107

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCGGAATTCT TACTTGCTCC GGGCAGACTC

30

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGAGGGCTCAG GAGGAGGTGG GTCTGGCGGT GGAGGTTCCG GCGGAGGCAG TTCAGAAGAC

60

GACATTGAGG CC

72

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

| | |
|---|----|
| GGCGGAGGTG GCTCAGGCGG AGGTGGATCT GGAGGTGGAG GCTCACGGCT TGAACAGCCC | 60 |
|---|----|

| | |
|-----|----|
| AAT | 63 |
|-----|----|

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

| | |
|---|----|
| TGAGCCTCCA CCTCCAGATC CACCTCCGCC TGAGCCACCT CCGCCAGTCT CTGTCAGCTC | 60 |
|---|----|

| | |
|-----|----|
| TGA | 63 |
|-----|----|

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

| | |
|--------------------------------------|----|
| CCGGAATTCT TAACTAGTCT CTGTCAGCTC TGA | 33 |
|--------------------------------------|----|

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Gly Ala Ser Ala Gly
1 5

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Gly Gly Ser Gly Gly
1 5

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Gly Gly Gly Ser Gly Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Ser
20 25

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro Arg
1 5 10 15
Thr Pro Pro Pro Ser
20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gly Gly Ser Gly Gly Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGAGGGCTCAG GAGGA

15

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Pro Gly Gly Ala Ile Ser Asn Met Tyr Ala Met
1 5 10

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Pro Gly Gly Ala Ile Ser Asn Met Tyr Ala Met Met Ile Ala Arg Phe
1 5 10 15
Lys Asn Phe Pro
20

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Pro Gly Gly Ala Ile Ser Asn Met Tyr Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Glu Arg Leu Glu
1

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Asp Pro Val Val His
1 5

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Gly Gly Gly Ser Gly
1 5

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Gly Gly Gly Ser Gly Gly Ser Gly
1 5

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids.
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu
1 5 10 15

Tyr Gly Thr Thr
20

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CATCGTGGAG GATGAT

16

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GAGGATGATT AAATG

15

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 20
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = threoninamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu
1 5 10 15

Tyr Gly Thr Xaa
20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 19
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = threoninamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr
1 5 10 15

Gly Thr Xaa

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = threoninamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr Gly
1 5 10 15

Thr Xaa

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = threoninamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr Gly Thr
1 5 10 15

Xaa

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = threoninamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr Gly Thr Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = threoninamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr Gly Thr Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 14
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = threoninamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr Gly Thr Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = threoninamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Pro Val Ile Lys Ala Arg Met Met Glu Tyr Gly Thr Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = threoninamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Val Ile Lys Ala Arg Met Met Glu Tyr Gly Thr Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = threoninamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ile Lys Ala Arg Met Met Glu Tyr Gly Thr Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 10
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = threoninamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Lys Ala Arg Met-Met Glu Tyr Gly Thr Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 18
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = threoninamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ser Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr
1 5 10 15
Gly Xaa

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = glycinamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Ser Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr
1 5 10 15

Xaa

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 16
(D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = tyrosinamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Ser Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 14
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = methioninamide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Ser Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = methioninamide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Ser Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = argininamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Ser Leu Ser Lys Val Ala Pro Val Ile Lys Ala Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = alaninamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Ser Leu Ser Lys Val Ala Pro Val Ile Lys Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = lysinamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Ser Leu Ser Lys Val Ala Pro Val Ile Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = isoleucinamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Ser Leu Ser Lys Val Ala Pro Val Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = glutamic acid amide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = glutamic acid amide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = glutamic acid amide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Val Ala Pro Val Ile Lys Ala Arg Met Met Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = glutamic acid amide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ala Pro Val Ile Lys Ala Arg Met Met Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = glutamic acid amide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Pro Val Ile Lys Ala Arg Met Met Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = methioninamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = methioninamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Ser Lys Val Ala Pro Val Ile Lys Ala Arg Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = argininamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Ser Lys Val Ala Pro Val Ile Lys Ala Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = alaninamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Ser Lys Val Ala Pro Val Ile Lys Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = glycinamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

| | | | | | | | | | | | | | | | |
|---------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Leu | Ser | Lys | Val | Ala | Pro | Val | Ile | Lys | Ala | Arg | Met | Met | Glu | Tyr |
| 1 | | | | | | | | | | | | | | | 15 |
| 5 10 | | | | | | | | | | | | | | | |

Xaa

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = tyrosinamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

| | | | | | | | | | | | | | | | |
|---------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Leu | Ser | Lys | Val | Ala | Pro | Val | Ile | Lys | Ala | Arg | Met | Met | Glu | Xaa |
| 1 | | | | | | | | | | | | | | | 15 |
| 5 10 | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = glutamic acid amide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Xaa
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = glycinamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr Xaa
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = tyrosinamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Xaa
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 14
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = glutamic acid amide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Leu Ser Lys Val-Ala Pro Val Ile Lys Ala Arg Met Met Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = glycinamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 14
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = tyrosinamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = lysinamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Ser Lys Val Ala Pro Val Ile Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Lys Pro Lys Ala Thr Ala Glu Gln Leu Lys Thr Val Met Asp Asp
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

ATC AAA GAA GAA CAT GTG ATC ATC CAG GCC GAG TTC TAT CTG AAT CCT
 Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu Phe Tyr Leu Asn Pro
 1 5 10 15

CAT GTG GAT ATG GCA AAG AAG GAG ACG GTC TGG CGG CTT GAA GAA TTT 144
 His Val Asp Met Ala Lys Lys Glu Thr Val Trp Arg Leu Glu Glu Phe
 35 40 45

GGA CGA TTT GCC AGC TTT GAG GCT CAA GGT GCA TTG GCC AAC ATA GCT 192
 Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala
 50 55 60

GTC GAC AAA GCC AAC CTG GAA ATC ATG ACA AAG CGC TCC AAC TAT ATG 240
 Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Met.
 65 70 75 80

ATC 243
Ile

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala
50 55 60

Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Met
 65 70 75 80

Ile

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

| | |
|---|-----|
| GAC GAA AAC CCA GTA GTG CAC TTC TTT AAA AAC ATC GTG ACT CCG CGT | 48 |
| Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro Arg | |
| 1 5 10 15 | |
| ACA CCC CCG CCA TCG GGA GGC GGG TCA GGT GGA TCC GGG GAC ACC CGA | 96 |
| Thr Pro Pro Pro Ser Gly Gly Ser Gly Ser Gly Asp Thr Arg | |
| 20 25 30 | |
| CCA CGT TTC CTG TGG CAG CCT AAAG AGG GAG TGT CAT TTC TTC AAT GGG | 144 |
| Pro Arg Phe Leu Trp Gln Pro Lys Arg Glu Cys His Phe Asn Gly | |
| 35 40 45 | |
| ACG GAG CGG GTG CGG TTC CTG GAC AGA TAC TTC TAT AAC CAG GAG GAG | 192 |
| Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu | |
| 50 55 60 | |
| TCC GTG CGT TTC GAC AGC GAC GTG GGG GAG TTC CGG GCG GTG ACG GAG | 240 |
| Ser Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu | |
| 65 70 75 80 | |
| CTG GGG CGG CCT GAC GCT GAG TAC TGG AAC AGC CAG AAG GAC ATC CTG | 288 |
| Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu | |
| 85 90 95 | |
| GAG CAG GCG CGG GCC GCG GTG GAC ACC TAC TGC AGA CAC AAC TAC GGG | 336 |
| Glu Gln Ala Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly | |
| 100 105 110 | |
| GTT GTG GAG AGC TTC ACA GTG CAG CGG GGA GCA TCA GCC GGC ATC AAA | 384 |
| Val Val Glu Ser Phe Thr Val Gln Arg Gly Ala Ser Ala Gly Ile Lys | |
| 115 120 125 | |
| GAA GAA CAT GTG ATC ATC CAG GCC GAG TTC TAT CTG AAT CCT GAC CAA | 432 |
| Glu Glu His Val Ile Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln | |
| 130 135 140 | |

| | |
|---|-----|
| TCA GGC GAA TTT ATG TTT GAC TTT GAT GGT GAT GAG ATT TTC CAT GTG | 480 |
| Ser Gly Glu Phe Met Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val | |
| 145 150 155 160 | |
| GAT ATG GCA AAG AAG GAG ACG GTC TGG CGG CTT GAA GAA TTT GGA CGA | 528 |
| Asp Met Ala Lys Lys Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg | |
| 165 170 175 | |
| TTT GCC AGC TTT GAG GCT CAA GGT GCA TTG GCC AAC ATA GCT GTG GAC | 576 |
| Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp | |
| 180 185 190 | |
| AAA GCC AAC CTG GAA ATC ATG ACA AAG CGC TCC AAC TAT ATG ATC | 621 |
| Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Met Ile | |
| 195 200 205 | |

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

| | |
|---|--|
| Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro Arg | |
| 1 5 10 15 | |
| Thr Pro Pro Pro Ser Gly Gly Ser Gly Gly Ser Gly Asp Thr Arg | |
| 20 25 30 | |
| Pro Arg Phe Leu Trp Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly | |
| 35 40 45 | |
| Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu | |
| 50 55 60 | |
| Ser Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu | |
| 65 70 75 80 | |
| Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu | |
| 85 90 95 | |
| Glu Gln Ala Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly | |
| 100 105 110 | |
| Val Val Glu Ser Phe Thr Val Gln Arg Gly Ala Ser Ala Gly Ile Lys | |
| 115 120 125 | |
| Glu Glu His Val Ile Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln | |
| 130 135 140 | |
| Ser Gly Glu Phe Met Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val | |
| 145 150 155 160 | |
| Asp Met Ala Lys Lys Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg | |
| 165 170 175 | |

Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp
 180 185 190

Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Met Ile
 195 200 205

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..273

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

| | |
|---|----|
| GGA GAC TCC GAA AGG CAT TTC GTG CAC CAG TTC AAG GGC GAG TGC TAC | 48 |
| Gly Asp Ser Glu Arg His Phe Val His Gln Phe Lys Gly Glu Cys Tyr | |
| 1 5 10 15 | |

| | |
|---|----|
| TTC ACC AAC GGG ACG CAG CGC ATA CGG CTC GTG ACC AGA TAC ATC TAC | 96 |
| Phe Thr Asn Gly Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr | |
| 20 25 30 | |

| | |
|---|-----|
| AAC CGG GAG GAG TAC CTG CGC TTC GAC AGC GAC GTG GGC GAG TAC CGC | 144 |
| Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg | |
| 35 40 45 | |

| | |
|---|-----|
| GCG GTG ACC GAG CTG GGG CGG CAC TCA GCC GAG TAC TAC AAT AAG CAG | 192 |
| Ala Val Thr Glu Leu Gly Arg His Ser Ala Glu Tyr Tyr Asn Lys Gln | |
| 50 55 60 | |

| | |
|---|-----|
| TAC CTG GAG CGA ACG CGG GCC GAG CTG GAC ACG GCG TGC AGA CAC AAC | 240 |
| Tyr Leu Glu Arg Thr Arg Ala Glu Leu Asp Thr Ala Cys Arg His Asn | |
| 65 70 75 80 | |

| | |
|---|-----|
| TAC GAG GAG ACG GAG GTC CCC ACC TCC CTG CGG | 273 |
| Tyr Glu Glu Thr Glu Val Pro Thr Ser Leu Arg | |
| 85 90 | |

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Gly Asp Ser Glu Arg His Phe Val His Gln Phe Lys Gly Glu Cys Tyr
 1 5 10 15

Phe Thr Asn Gly Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr
 20 25 30

Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg
 35 40 45

Ala Val Thr Glu Leu Gly Arg His Ser Ala Glu Tyr Tyr Asn Lys Gln
 50 55 60

Tyr Leu Glu Arg Thr Arg Ala Glu Leu Asp Thr Ala Cys Arg His Asn
 65 70 75 80

Tyr Glu Glu Thr Glu Val Pro Thr Ser Leu Arg
 85 90

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT 48
 Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val
 1 5 10 15

TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT 96
 Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly
 20 25 30

GAT GAG TTG TTC TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG 144
 Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg
 35 40 45

CTT CCT GAG TTT GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG 192
 Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu
 50 55 60

CAA AAC ATA GCT GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG 240
 Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg
 65 70 75 80

TCA AAT TTC ACC CCA GCT ACT
 Ser Asn Phe Thr Pro Ala Thr
 85

261

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val
 1 5 10 15

Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly
 20 25 30

Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg
 35 40 45

Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu
 50 55 60

Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg
 65 70 75 80

Ser Asn Phe Thr Pro Ala Thr
 85

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AGT CGC CTC TCG AAG GTG GCT CCA GTG ATT AAA GCC AGA ATG ATG GAG
 Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu
 1 5 10 15

48

TAT GGA ACC ACA GGA GGT GGA GGC TCT GGA GGT GGA GGC TCA GGA GGA
 Tyr Gly Thr Thr Gly Gly Ser Gly Gly Gly Ser Gly Gly
 20 25 30

96

| | | | | |
|--|-----|-----|-----|-----|
| GGT GGG TCC GGA GAC TCC GAA AGG CAT TTC GTG CAC CAG TTC AAG GGC Gly Gly Ser Gly Asp Ser Glu Arg His Phe Val His Gln Phe Lys Gly | 35 | 40 | 45 | 144 |
| GAG TGC TAC TTC ACC AAC GGG ACG CAG CGC ATA CGG CTC GTG ACC AGA Glu Cys Tyr Phe Thr Asn Gly Thr Gln Arg Ile Arg Leu Val Thr Arg | 50 | 55 | 60 | 192 |
| TAC ATC TAC AAC CGG GAG GAG TAC CTG CGC TTC GAC AGC GAC GTG GGC Tyr Ile Tyr Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly | 65 | 70 | 75 | 240 |
| GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CAC TCA GCC GAG TAC TAC Glu Tyr Arg Ala Val Thr Glu Leu Gly Arg His Ser Ala Glu Tyr Tyr | 85 | 90 | 95 | 288 |
| AAT AAG CAG TAC CTG GAG CGA ACG CGG GCC GAG CTG GAC ACG GCG TGC Asn Lys Gln Tyr Leu Glu Arg Thr Arg Ala Glu Leu Asp Thr Ala Cys | 100 | 105 | 110 | 336 |
| AGA CAC AAC TAC GAG GAG ACG GAG GTC CCC ACC TCC CTG CGG GGT GGA Arg His Asn Tyr Glu Glu Thr Glu Val Pro Thr Ser Leu Arg Gly Gly | 115 | 120 | 125 | 384 |
| TCA GGT GGC GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC TTC TAT GGT Ser Gly Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly | 130 | 135 | 140 | 432 |
| ACA ACT GTT TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu | 145 | 150 | 155 | 480 |
| TTT GAT GGT GAT GAG TTG TTC TAT GTG GAC TTG GAT AAG AAG AAA ACT Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Thr | 165 | 170 | 175 | 528 |
| GTC TGG AGG CTT CCT GAG TTT GGC CAA TTG ATA CTC TTT GAG CCC CAA Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln | 180 | 185 | 190 | 576 |
| GGT GGA CTG CAA AAC ATA GCT GCA GAA AAA CAC AAC TTG GGA ATC TTG Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu | 195 | 200 | 205 | 624 |
| ACT AAG AGG TCA AAT TTC ACC CCA GCT ACT Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr | 210 | 215 | | 654 |

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 218 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu
 1 5 10 15

Tyr Gly Thr Thr Gly Gly Ser Gly Gly Gly Ser Gly Gly
 20 25 30

Gly Gly Ser Gly Asp Ser Glu Arg His Phe Val His Gln Phe Lys Gly
 35 40 45

Glu Cys Tyr Phe Thr Asn Gly Thr Gln Arg Ile Arg Leu Val Thr Arg
 50 55 60

Tyr Ile Tyr Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly
 65 70 75 80

Glu Tyr Arg Ala Val Thr Glu Leu Gly Arg His Ser Ala Glu Tyr Tyr
 85 90 95

Asn Lys Gln Tyr Leu Glu Arg Thr Arg Ala Glu Leu Asp Thr Ala Cys
 100 105 110

Arg His Asn Tyr Glu Glu Thr Glu Val Pro Thr Ser Leu Arg Gly Gly
 115 120 125

Ser Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly
 130 135 140

Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu
 145 150 155 160

Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Thr
 165 170 175

Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln
 180 185 190

Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu
 195 200 205

Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr
 210 215

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

| | |
|---|-----|
| GGA GAC TCC GAA AGG CAT TTC GTG TTC CAG TTC AAG GGC GAG TGC TAC Gly Asp Ser Glu Arg His Phe Val Phe Gln Phe Lys Gly Glu Cys Tyr 1 5 10 15 | 48 |
| TTC ACC AAC GGG ACG CAG CGC ATA CGA TCT GTG GAC AGA TAC ATC TAC Phe Thr Asn Gly Thr Gln Arg Ile Arg Ser Val Asp Arg Tyr Ile Tyr 20 25 30 | 96 |
| AAC CGG GAG GAG TAC CTG CGC TTC GAC AGC GAC GTG GGC GAG TAC CGC Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg 35 40 45 | 144 |
| GCG GTG ACC GAG CTG GGG CGG CCA GAC CCC GAG TAC TAC AAT AAG CAG Ala Val Thr Glu Leu Gly Arg Pro Asp Pro Glu Tyr Tyr Asn Lys Gln 50 55 60 | 192 |
| TAC CTG GAG CAA ACG CGG GCC GAG CTG GAC ACG GTG TGC AGA CAC AAC Tyr Leu Glu Gln Thr Arg Ala Glu Leu Asp Thr Val Cys Arg His Asn 65 70 75 80 | 240 |
| TAC GAG GGG GTG GAG ACC CAC ACC TCC CTG CGG Tyr Glu Gly Val Glu Thr His Thr Ser Leu Arg 85 90 | 273 |

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

| |
|--|
| Gly Asp Ser Glu Arg His Phe Val Phe Gln Phe Lys Gly Glu Cys Tyr 1 5 10 15 |
| Phe Thr Asn Gly Thr Gln Arg Ile Arg Ser Val Asp Arg Tyr Ile Tyr 20 25 30 |
| Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg 35 40 45 |
| Ala Val Thr Glu Leu Gly Arg Pro Asp Pro Glu Tyr Tyr Asn Lys Gln 50 55 60 |
| Tyr Leu Glu Gln Thr Arg Ala Glu Leu Asp Thr Val Cys Arg His Asn 65 70 75 80 |
| Tyr Glu Gly Val Glu Thr His Thr Ser Leu Arg 85 90 |

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC GTC TAT GGT ACA ACT GTA
 Glu Asp Asp Ile Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val
 1 5 10 15

48

TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT
 Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly
 20 25 30

96

GAT GAG TGG TTC TAT GTG GAC TTG GAT AAG AAG GAG ACT ATC TGG ATG
 Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met
 35 40 45

144

CTT CCT GAG TTT GGC CAA TTG ACA AGC TTT GAC CCC CAA GGT GGA CTG
 Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu
 50 55 60

192

CAA AAC ATA GCT ACA GGA AAA TAC ACC TTG GGA ATC TTG ACT AAG AGG
 Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg
 65 70 75 80

240

TCA AAT TCC ACC CCA GCT ACT
 Ser Asn Ser Thr Pro Ala Thr
 85

261

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Glu Asp Asp Ile Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val
 1 5 10 15

Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly
 20 25 30

| | | |
|---|----|----|
| Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met | | |
| 35 | 40 | 45 |
| Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu | | |
| 50 | 55 | 60 |
| Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg | | |
| 65 | 70 | 75 |
| Ser Asn Ser Thr Pro Ala Thr | | |
| 85 | | |

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

| | |
|---|-----|
| TTC TTT AAA AAC ATC GTG ACT CCG CGT ACA CCC CCG CCA GGA GGT GGA | 48 |
| Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Gly Gly Gly | |
| 1 5 10 15 | |
| GGC TCT GGA GGT GGA GGC TCA GGA GGA GGT GGG TCC GGA GAC TCC GAA | 96 |
| Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Ser Glu | |
| 20 25 30 | |
| AGG CAT TTC GTG TTC CAG TTC AAG GGC GAG TGC TAC TTC ACC AAC GGG | 144 |
| Arg His Phe Val Phe Gln Phe Lys Gly Glu Cys Tyr Phe Thr Asn Gly | |
| 35 40 45 | |
| ACG CAG CGC ATA CGA TCT GTG GAC AGA TAC ATC TAC AAC CGG GAG GAG | 192 |
| Thr Gln Arg Ile Arg Ser Val Asp Arg Tyr Ile Tyr Asn Arg Glu Glu | |
| 50 55 60 | |
| TAC CTG CGC TTC GAC AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG | 240 |
| Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu | |
| 65 70 75 80 | |
| CTG GGG CGG CCA GAC CCC GAG TAC TAC AAT AAG CAG TAC CTG GAG CAA | 288 |
| Leu Gly Arg Pro Asp Pro Glu Tyr Tyr Asn Lys Gln Tyr Leu Glu Gln | |
| 85 90 95 | |
| ACG CGG GCC GAG CTG GAC ACG GTG TGC AGA CAC AAC TAC GAG GGG GTG | 336 |
| Thr Arg Ala Glu Leu Asp Thr Val Cys Arg His Asn Tyr Glu Gly Val | |
| 100 105 110 | |

| | |
|---|-----|
| GAG ACC CAC ACC TCC CTG CGG GGT GGA TCA GGT GGC GAA GAC GAC ATT Glu Thr His Thr Ser Leu Arg Gly Gly Ser Gly Gly Glu Asp Asp Ile 115 120 125 | 384 |
| GAG GCC GAC CAC GTA GGC GTC TAT GGT ACA ACT GTA TAT CAG TCT CCT Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro 130 135 140 | 432 |
| GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TGG TTC Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Trp Phe 145 150 155 160 | 480 |
| TAT GTG GAC TTG GAT AAG AAG GAG ACT ATC TGG ATG CTT CCT GAG TTT Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met Leu Pro Glu Phe 165 170 175 | 528 |
| GGC CAA TTG ACA AGC TTT GAC CCC CAA GGT GGA CTG CAA AAC ATA GCT Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Leu Gln Asn Ile Ala 180 185 190 | 576 |
| ACA GGA AAA TAC ACC TTG GGA ATC TTG ACT AAG AGG TCA AAT TCC ACC Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr 195 200 205 | 624 |
| CCA GCT ACT Pro Ala Thr 210 | 633 |

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

| |
|--|
| Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Gly Gly Gly 1 5 10 15 |
| Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Asp Ser Glu 20 25 30 |
| Arg His Phe Val Phe Gln Phe Lys Gly Glu Cys Tyr Phe Thr Asn Gly 35 40 45 |
| Thr Gln Arg Ile Arg Ser Val Asp Arg Tyr Ile Tyr Asn Arg Glu Glu 50 55 60 |
| Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu 65 70 75 80 |
| Leu Gly Arg Pro Asp Pro Glu Tyr Tyr Asn Lys Gln Tyr Leu Glu Gln 85 90 95 |
| Thr Arg Ala Glu Leu Asp Thr Val Cys Arg His Asn Tyr Glu Gly Val ~ 100 105 110 |

Glu Thr His Thr Ser Leu Arg Gly Gly Ser Gly Gly Glu Asp Asp Ile
 115 120 125
 Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro
 130 135 140
 Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Trp Phe
 145 150 155 160
 Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met Leu Pro Glu Phe
 165 170 175
 Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala
 180 185 190
 Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr
 195 200 205
 Pro Ala Thr
 210

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

| | |
|---|-----|
| CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC AGG ACA GAG GCC | 48 |
| Arg Leu Glu Gln Pro Asn Val Ala Ile Ser Leu Ser Arg Thr Glu Ala | |
| 1 5 10 15 | |
| CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA GAT TTC TAC CCA | 96 |
| Leu Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro | |
| 20 25 30 | |
| GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG GAG GAG ACA GTG | 144 |
| Ala Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr Val | |
| 35 40 45 | |
| GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC TGG ACC TTC CAG | 192 |
| Gly Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln | |
| 50 55 60 | |
| GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA GAG GTC TAC ACC | 240 |
| Val Leu Val Met Leu Glu Met Thr Pro His Gln Gly Glu Val Tyr Thr | |
| 65 70 75 80 | |

TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC ACT GTG GAG TGG 288
 Cys His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp
 85 90 95

AGG GCA CAG TCC GAG TCT GCC CGG 312
 Arg Ala Gln Ser Glu Ser Ala Arg
 100

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Arg Leu Glu Gln Pro Asn Val Ala Ile Ser Leu Ser Arg Thr Glu Ala
 1 5 10 15

Leu Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro
 20 25 30

Ala Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr Val
 35 40 45

Gly Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln
 50 55 60

Val Leu Val Met Leu Glu Met Thr Pro His Gln Gly Glu Val Tyr Thr
 65 70 75 80

Cys His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp
 85 90 95

Arg Ala Gln Ser Glu Ser Ala Arg
 100

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

| | |
|---|-----|
| GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val 1 5 10 15 | 48 |
| TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly 20 25 30 | 96 |
| GAT GAG TTG TTC TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg 35 40 45 | 144 |
| CTT CCT GAG TTT GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu 50 55 60 | 192 |
| CAA AAC ATA GCT GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg 65 70 75 80 | 240 |
| TCA AAT TTC ACC CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC Ser Asn Phe Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe 85 90 95 | 288 |
| CCC AAG TCC CCT GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe 100 105 110 | 336 |
| GTG GAC AAC ATC TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT Val Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn 115 120 125 | 384 |
| AGC AAG TCA GTC ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC Ser Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn 130 135 140 | 432 |
| CGT GAC CAT TCC TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT Arg Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser 145 150 155 160 | 480 |
| GAT GAT GAC ATT TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu 165 170 175 | 528 |
| CCG GTT CTG AAA CAC TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG Pro Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu 180 185 190 | 576 |
| CTG ACA GAG ACT Leu Thr Glu Thr 195 | 588 |

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 196 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Asp | Asp | Ile | Glu | Ala | Asp | His | Val | Gly | Phe | Tyr | Gly | Thr | Thr | Val |
| 1 | | | | | | | | | | | | | | | 15 |
| | | | | 5 | | | | | | | | | | | |
| Tyr | Gln | Ser | Pro | Gly | Asp | Ile | Gly | Gln | Tyr | Thr | His | Glu | Phe | Asp | Gly |
| | | | | | | | | | | | | | | | 30 |
| | | | | 20 | | | | 25 | | | | | | | |
| Asp | Glu | Leu | Phe | Tyr | Val | Asp | Leu | Asp | Lys | Lys | Lys | Thr | Val | Trp | Arg |
| | | | | | | | | | | | | | | | 45 |
| | | | | | | | | 35 | | 40 | | | | | |
| Leu | Pro | Glu | Phe | Gly | Gln | Leu | Ile | Leu | Phe | Glu | Pro | Gln | Gly | Gly | Leu |
| | | | | | | | | 50 | | 55 | | | | | 60 |
| | | | | | | | | | | | | | | | |
| Gln | Asn | Ile | Ala | Ala | Glu | Lys | His | Asn | Leu | Gly | Ile | Leu | Thr | Lys | Arg |
| | | | | | | | | 65 | | 70 | | | | | 80 |
| | | | | | | | | | | | | | | | |
| Ser | Asn | Phe | Thr | Pro | Ala | Thr | Asn | Glu | Ala | Pro | Gln | Ala | Thr | Val | Phe |
| | | | | | | | | 85 | | 90 | | | | | 95 |
| | | | | | | | | | | | | | | | |
| Pro | Lys | Ser | Pro | Val | Leu | Leu | Gly | Gln | Pro | Asn | Thr | Leu | Ile | Cys | Phe |
| | | | | | | | | 100 | | 105 | | | | | 110 |
| | | | | | | | | | | | | | | | |
| Val | Asp | Asn | Ile | Phe | Pro | Pro | Val | Ile | Asn | Ile | Thr | Trp | Leu | Arg | Asn |
| | | | | | | | | 115 | | 120 | | | | | 125 |
| | | | | | | | | | | | | | | | |
| Ser | Lys | Ser | Val | Thr | Asp | Gly | Val | Tyr | Glu | Thr | Ser | Phe | Leu | Val | Asn |
| | | | | | | | | 130 | | 135 | | | | | 140 |
| | | | | | | | | | | | | | | | |
| Arg | Asp | His | Ser | Phe | His | Lys | Leu | Ser | Tyr | Leu | Thr | Phe | Ile | Pro | Ser |
| | | | | | | | | 145 | | 150 | | | | | 160 |
| | | | | | | | | | | | | | | | |
| Asp | Asp | Asp | Ile | Tyr | Asp | Cys | Lys | Val | Glu | His | Trp | Gly | Leu | Glu | Glu |
| | | | | | | | | 165 | | 170 | | | | | 175 |
| | | | | | | | | | | | | | | | |
| Pro | Val | Leu | Lys | His | Trp | Glu | Pro | Glu | Ile | Pro | Ala | Pro | Met | Ser | Glu |
| | | | | | | | | | 180 | | 185 | | | | 190 |
| | | | | | | | | | | | | | | | |
| Leu | Thr | Glu | Thr | | | | | | | | | | | | |
| | | | 195 | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

| | |
|---|-----|
| AGT CGC CTC TCG AAG GTG GCT CCA GTG ATT AAA GCC AGA ATG ATG GAG Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu 1 5 10 15 | 48 |
| TAT GGA ACC ACA GGA GGT GGA GGC TCT GGA GGT GGA GGC TCA GGA GGA Tyr Gly Thr Thr Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly 20 25 30 | 96 |
| GGT GGG TCC GGA GAC TCC GAA AGG CAT TTC GTG CAC CAG TTC AAG GGC Gly Gly Ser Gly Asp Ser Glu Arg His Phe Val His Gln Phe Lys Gly 35 40 45 | 144 |
| GAG TGC TAC TTC ACC AAC GGG ACG CAG CGC ATA CGG CTC GTG ACC AGA Glu Cys Tyr Phe Thr Asn Gly Thr Gln Arg Ile Arg Leu Val Thr Arg 50 55 60 | 192 |
| TAC ATC TAC AAC CGG GAG GAG TAC CTG CGC TTC GAC AGC GAC GTG GGC Tyr Ile Tyr Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly 65 70 75 80 | 240 |
| GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CAC TCA GCC GAG TAC TAC Glu Tyr Arg Ala Val Thr Glu Leu Gly Arg His Ser Ala Glu Tyr Tyr 85 90 95 | 288 |
| AAT AAG CAG TAC CTG GAG CGA ACG CGG GCC GAG CTG GAC ACG GCG TGC Asn Lys Gln Tyr Leu Glu Arg Thr Arg Ala Glu Leu Asp Thr Ala Cys 100 105 110 | 336 |
| AGA CAC AAC TAC GAG GAG ACG GAG GTC CCC ACC TCC CTG CGG GGT GGA Arg His Asn Tyr Glu Glu Thr Glu Val Pro Thr Ser Leu Arg Gly Gly 115 120 125 | 384 |
| TCA GGT GGC GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC TTC TAT GGT Ser Gly Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly 130 135 140 | 432 |
| ACA ACT GTT TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu 145 150 155 160 | 480 |
| TTT GAT GGT GAT GAG TTG TTC TAT GTG GAC TTG GAT AAG AAG AAA ACT Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Thr 165 170 175 | 528 |
| GTC TGG AGG CTT CCT GAG TTT GGC CAA TTG ATA CTC TTT GAG CCC CAA Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln 180 185 190 | 576 |
| GGT GGA CTG CAA AAC ATA GCT GCA GAA AAA CAC AAC TTG GGA ATC TTG Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu 195 200 205 | 624 |
| ACT AAG AGG TCA AAT TTC ACC CCA GCT ACC AAT GAG GCT CCT CAA GCG Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala 210 215 220 | 672 |
| ACT GTG TTC CCC AAG TCC CCT GTG CTG CTG GGT CAG CCC AAC ACC CTT Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu 225 230 235 240 | 720 |

| | |
|---|------|
| ATC TGC TTT GTG GAC AAC ATC TTC CCA CCT GTG ATC AAC ATC ACA TGG Ile Cys Phe Val Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp 245 250 255 | 768 |
| CTC AGA AAT AGC AAG TCA GTC ACA GAC GGC GTT TAT GAG ACC AGC TTC Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe 260 265 270 | 816 |
| CTC GTC AAC CGT GAC CAT TCC TTC CAC AAG CTG TCT TAT CTC ACC TTC Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe 275 280 285 | 864 |
| ATC CCT TCT GAT GAT GAC ATT TAT GAC TGC AAG GTG GAG CAC TGG GGC Ile Pro Ser Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly 290 295 300 | 912 |
| CTG GAG GAG CCG GTT CTG AAA CAC TGG GAA CCT GAG ATT CCA GCC CCC Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro 305 310 315 320 | 960 |
| ATG TCA GAG CTG ACA GAG ACT GGC GGA GGT GGC TCA GGC GGA GGT GGA Met Ser Glu Leu Thr Glu Thr Gly Gly Ser Gly Gly Gly Gly 325 330 335 | 1008 |
| TCT GGA GGT GGA GGC TCA CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC Ser Gly Gly Gly Ser Arg Leu Glu Gln Pro Asn Val Ala Ile Ser 340 345 350 | 1056 |
| CTG TCC AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG Leu Ser Arg Thr Glu Ala Leu Asn His His Asn Thr Leu Val Cys Ser 355 360 365 | 1104 |
| GTG ACA GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT Val Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg Trp Phe Arg Asn 370 375 380 | 1152 |
| GGC CAG GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT Gly Gln Glu Glu Thr Val Gly Val Ser Ser Thr Gln Leu Ile Arg Asn 385 390 395 400 | 1200 |
| GGG GAC TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT Gly Asp Trp Thr Phe Gln Val Leu Val Met Leu Glu Met Thr Pro His 405 410 415 | 1248 |
| CAG GGA GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC Gln Gly Glu Val Tyr Thr Cys His Val Glu His Pro Ser Leu Lys Ser 420 425 430 | 1296 |
| CCC ATC ACT GTG GAG TGG AGG GCA CAG TCC GAG TCT GCC CGG AGC AAG Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser Ala Arg Ser Lys 435 440 445 | 1344 |

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 448 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu
 1 5 10 15

Tyr Gly Thr Thr Gly Gly Ser Gly Gly Ser Gly Gly 20 25 30

Gly Gly Ser Gly Asp Ser Glu Arg His Phe Val His Gln Phe Lys Gly
 35 40 45

Glu Cys Tyr Phe Thr Asn Gly Thr Gln Arg Ile Arg Leu Val Thr Arg
 50 55 60

Tyr Ile Tyr Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly
 65 70 75 80

Glu Tyr Arg Ala Val Thr Glu Leu Gly Arg His Ser Ala Glu Tyr Tyr
 85 90 95

Asn Lys Gln Tyr Leu Glu Arg Thr Arg Ala Glu Leu Asp Thr Ala Cys
 100 105 110

Arg His Asn Tyr Glu Glu Thr Glu Val Pro Thr Ser Leu Arg Gly Gly
 115 120 125

Ser Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly
 130 135 140

Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu
 145 150 155 160

Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr
 165 170 175

Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln
 180 185 190

Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu
 195 200 205

Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala
 210 215 220

Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu
 225 230 235 240

Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp
 245 250 255

Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe
 260 265 270

Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe
 275 280 285

Ile Pro Ser Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly
 290 295 300

Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro
 305 310 315 320

Met Ser Glu Leu Thr Glu Thr Gly Gly Gly Ser Gly Gly Gly Gly
 325 330 335
 Ser Gly Gly Gly Ser Arg Leu Glu Gln Pro Asn Val Ala Ile Ser
 340 345 350
 Leu Ser Arg Thr Glu Ala Leu Asn His His Asn Thr Leu Val Cys Ser
 355 360 365
 Val Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg Trp Phe Arg Asn
 370 375 380
 Gly Gln Glu Glu Thr Val Gly Val Ser Ser Thr Gln Leu Ile Arg Asn
 385 390 395 400
 Gly Asp Trp Thr Phe Gln Val Leu Val Met Leu Glu Met Thr Pro His
 405 410 415
 Gln Gly Glu Val Tyr Thr Cys His Val Glu His Pro Ser Leu Lys Ser
 420 425 430
 Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser Ala Arg Ser Lys
 435 440 445

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

| | |
|---|-----|
| CGG CTT GAA CAG CCC AAT GTC GTC ATC TCC CTG TCC AGG ACA GAG GCC | 48 |
| Arg Leu Glu Gln Pro Asn Val Val Ile Ser Leu Ser Arg Thr Glu Ala | |
| 1 5 10 15 | |
| CTC AAC CAC CAC AAC ACT CTG GTC TGC TCA GTG ACA GAT TTC TAC CCA | 96 |
| Leu Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro | |
| 20 25 30 | |
| GCC AAG ATC AAA GTG CGC TGG TTC CGG AAT GGC CAG GAG GAG ACG GTG | 144 |
| Ala Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr Val | |
| 35 40 45 | |
| GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC TGG ACC TTC CAG | 192 |
| Gly Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln | |
| 50 55 60 | |

| | |
|---|-----|
| GTC CTG GTC ATG CTG GAG ATG ACC CCT CGG CGG GGA GAG GTC TAC ACC | 240 |
| Val Leu Val Met Leu Glu Met Thr Pro Arg Arg Gly Glu Val Tyr Thr | |
| 65 70 75 80 | |
| TGC CAC GTG GAG CAT CCG AGC CTG AAG AGC CCC ATC ACT GTG GAG TGG | 288 |
| Cys His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp | |
| 85 90 95 | |
| AGG GCA CAG TCT GAG TCT GCC CGG AGC AAG | 318 |
| Arg Ala Gln Ser Glu Ser Ala Arg Ser Lys | |
| 100 105 | |

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

| | |
|---|--|
| Arg Leu Glu Gln Pro Asn Val Val Ile Ser Leu Ser Arg Thr Glu Ala | |
| 1 5 10 15 | |
| Leu Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro | |
| 20 25 30 | |
| Ala Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr Val | |
| 35 40 45 | |
| Gly Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln | |
| 50 55 60 | |
| Val Leu Val Met Leu Glu Met Thr Pro Arg Arg Gly Glu Val Tyr Thr | |
| 65 70 75 80 | |
| Cys His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp | |
| 85 90 95 | |
| Arg Ala Gln Ser Glu Ser Ala Arg Ser Lys | |
| 100 105 | |

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

| | |
|--|-----|
| TTC TTT AAA AAC ATC GTG ACT CCG CGT ACA CCC CCG CCA GGA GGT GGA Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Gly Gly Gly | 48 |
| 1 5 10 15 | |
| GGC TCT GGA GGT GGA GGC TCA GGA GGA GGT GGG TCC GGA GAC TCC GAA Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Asp Ser Glu | 96 |
| 20 25 30 | |
| AGG CAT TTC GTG TTC CAG TTC AAG GGC GAG TGC TAC TTC ACC AAC GGG Arg His Phe Val Phe Gln Phe Lys Gly Glu Cys Tyr Phe Thr Asn Gly | 144 |
| 35 40 45 | |
| ACG CAG CGC ATA CGA TCT GTG GAC AGA TAC ATC TAC AAC CGG GAG GAG Thr Gln Arg Ile Arg Ser Val Asp Arg Tyr Ile Tyr Asn Arg Glu Glu | 192 |
| 50 55 60 | |
| TAC CTG CGC TTC GAC AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu | 240 |
| 65 70 75 80 | |
| CTG GGG CGG CCA GAC CCC GAG TAC TAC AAT AAG CAG TAC CTG GAG CAA Leu Gly Arg Pro Asp Pro Glu Tyr Tyr Asn Lys Gln Tyr Leu Glu Gln | 288 |
| 85 90 95 | |
| ACG CGG GCC GAG CTG GAC ACG GTG TGC AGA CAC AAC TAC GAG GGG GTG Thr Arg Ala Glu Leu Asp Thr Val Cys Arg His Asn Tyr Glu Gly Val | 336 |
| 100 105 110 | |
| GAG ACC CAC ACC TCC CTG CGG GGT GGA TCA GGT GGC GAA GAC GAC ATT Glu Thr His Thr Ser Leu Arg Gly Ser Gly Gly Glu Asp Asp Ile | 384 |
| 115 120 125 | |
| GAG GCC GAC CAC GTA GGC GTC TAT GGT ACA ACT GTA TAT CAG TCT CCT Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro | 432 |
| 130 135 140 | |
| GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TGG TTC Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Trp Phe | 480 |
| 145 150 155 160 | |
| TAT GTG GAC TTG GAT AAG AAG GAG ACT ATC TGG ATG CTT CCT GAG TTT Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met Leu Pro Glu Phe | 528 |
| 165 170 175 | |
| GGC CAA TTG ACA AGC TTT GAC CCC CAA GGT GGA CTG CAA AAC ATA GCT Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala | 576 |
| 180 185 190 | |
| ACA GGA AAA TAC ACC TTG GGA ATC TTG ACT AAG AGG TCA AAT TCC ACC Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr | 624 |
| 195 200 205 | |
| CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro | 672 |
| 210 215 220 | |
| GTG CTG CTG GGT CAG CCC AAA ACC CTT ATC TGC TTT GTG GAC AAC ATC Val Leu Leu Gly Gln Pro Lys Thr Leu Ile Cys Phe Val Asp Asn Ile | 720 |
| 225 230 235 240 | |

| | |
|---|------|
| TTC CCT CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val 245 250 255 | 768 |
| ACA GAC GGC GTT TAT GAG ACC AGC TTC CTT GTC AAC CGT GAC CAT TCC Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser 260 265 270 | 816 |
| TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAC GAT GAT ATT Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile 275 280 285 | 864 |
| TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Pro Val Leu Lys 290 295 300 | 912 |
| CAT TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG CTG ACA GAG ACT His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr 305 310 315 320 | 960 |
| GGC GGA GGT GGC TCA GGC GGA GGT GGA TCT GGA GGT GGA GGC TCA CGG Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Arg 325 330 335 | 1008 |
| CTT GAA CAG CCC AAT GTC GTC ATC TCC CTG TCC AGG ACA GAG GCC CTC Leu Glu Gln Pro Asn Val Val Ile Ser Leu Ser Arg Thr Glu Ala Leu 340 345 350 | 1056 |
| AAC CAC CAC AAC ACT CTG GTC TGC TCA GTG ACA GAT TTC TAC CCA GCC Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro Ala 355 360 365 | 1104 |
| AAG ATC AAA GTG CGC TGG TTC CGG AAT GGC CAG GAG GAG ACG GTG GGG Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr Val Gly 370 375 380 | 1152 |
| GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC TGG ACC TTC CAG GTC Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln Val 385 390 395 400 | 1200 |
| CTG GTC ATG CTG GAG ATG ACC CCT CGG CGG GGA GAG GTC TAC ACC TGC Leu Val Met Leu Glu Met Thr Pro Arg Arg Gly Glu Val Tyr Thr Cys 405 410 415 | 1248 |
| CAC GTG GAG CAT CCG AGC CTG AAG AGC CCC ATC ACT GTG GAG TGG AGG His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp Arg 420 425 430 | 1296 |
| GCA CAG TCT GAG TCT GCC CGG AGC AAG Ala Gln Ser Glu Ser Ala Arg Ser Lys 435 440 | 1323 |

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Gly Gly Gly
 1 5 10 15

Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Asp Ser Glu
 20 25 30

Arg His Phe Val Phe Gln Phe Lys Gly Glu Cys Tyr Phe Thr Asn Gly
 35 40 45

Thr Gln Arg Ile Arg Ser Val Asp Arg Tyr Ile Tyr Asn Arg Glu Glu
 50 55 60

Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu
 65 70 75 80

Leu Gly Arg Pro Asp Pro Glu Tyr Tyr Asn Lys Gln Tyr Leu Glu Gln
 85 90 95

Thr Arg Ala Glu Leu Asp Thr Val Cys Arg His Asn Tyr Glu Gly Val
 100 105 110

Glu Thr His Thr Ser Leu Arg Gly Gly Ser Gly Gly Glu Asp Asp Ile
 115 120 125

Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro
 130 135 140

Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Trp Phe
 145 150 155 160

Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met Leu Pro Glu Phe
 165 170 175

Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala
 180 185 190

Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr
 195 200 205

Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro
 210 215 220

Val Leu Leu Gly Gln Pro Lys Thr Leu Ile Cys Phe Val Asp Asn Ile
 225 230 235 240

Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val
 245 250 255

Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser
 260 265 270

Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile
 275 280 285

Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys
 290 295 300

His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr
 305 310 315 320

Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Arg
325 330 335

Leu Glu Gln Pro Asn Val Val Ile Ser Leu Ser Arg Thr Glu Ala Leu
340 345 350

Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro Ala
355 360 365

Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr Val Gly
370 375 380

Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln Val
385 390 395 400

Leu Val Met Leu Glu Met Thr Pro Arg Arg Gly Glu Val Tyr Thr Cys
405 410 415

His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp Arg
420 425 430

Ala Gln Ser Glu Ser Ala Arg Ser Lys
435 440

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC GTC TAT GGT ACA ACT GTA
Glu Asp Asp Ile Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val
1 5 10 15

TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT
Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly
20 25 30

GAT GAG TGG TTC TAT GTG GAC TTG GAT AAG AAG GAG ACT ATC TGG ATG
Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met
35 40 45

CTT CCT GAG TTT GGC CAA TTG ACA AGC TTT GAC CCC CAA GGT GGA CTG
Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu
50 55 60

48

96

144

192

| | |
|---|-----|
| CAA AAC ATA GCT ACA GGA AAA TAC ACC TTG GGA ATC TTG ACT AAG AGG Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg 65 70 75 80 | 240 |
| TCA AAT TCC ACC CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC Ser Asn Ser Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe 85 90 95 | 288 |
| CCC AAG TCC CCT GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe 100 105 110 | 336 |
| GTG GAC AAC ATC TTC CCT CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT Val Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn 115 120 125 | 384 |
| AGC AAG TCA GTC ACA GAC GGC GTT TAT GAG ACC AGC TTC CTT GTC AAC Ser Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn 130 135 140 | 432 |
| CGT GAC CAT TCC TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT Arg Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser 145 150 155 160 | 480 |
| GAC GAT GAT ATT TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu 165 170 175 | 528 |
| CCG GTT CTG AAA CAC TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG Pro Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu 180 185 190 | 576 |
| CTG ACA GAG ACT Leu Thr Glu Thr 195 | 588 |

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

| |
|--|
| Glu Asp Asp Ile Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val 1 5 10 15 |
| Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly 20 25 30 |
| Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met 35 40 45 |
| Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu 50 55 60 |

Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg
 65 70 75 80
 Ser Asn Ser Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe
 85 90 95
 Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe
 100 105 110
 Val Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn
 115 120 125
 Ser Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn
 130 135 140
 Arg Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser
 145 150 155 160
 Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu
 165 170 175
 Pro Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu
 180 185 190
 Leu Thr Glu Thr
 195

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 702 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

| | |
|---|-----|
| TTC TTT AAA AAC ATC GTG ACT CCG CGT ACA CCC CCG CCA GGA GGT GGA | 48 |
| Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Gly Gly Gly | |
| 1 5 10 15 | |
| Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly Gly | 96 |
| 20 25 30 | |
| TCC GGC GGA GGC GGT TCA GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC | 144 |
| Ser Gly Gly Gly Ser Glu Asp Asp Ile Glu Ala Asp His Val Gly | |
| 35 40 45 | |
| GTC TAT GGT ACA ACT GTA TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC | 192 |
| Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr | |
| 50 55 60 | |

| | |
|---|-----|
| ACA CAT GAA TTT GAT GGT GAT GAG TGG TTC TAT GTG GAC TTG GAT AAG | 240 |
| Thr His Glu Phe Asp Gly Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys | |
| 65 70 75 80 | |
| AAG GAG ACT ATC TGG ATG CTT CCT GAG TTT GGC CAA TTG ACA AGC TTT | 288 |
| Lys Glu Thr Ile Trp Met Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe | |
| 85 90 95 | |
| GAC CCC CAA GGT GGA CTG CAA AAC ATA GCT ACA GGA AAA TAC ACC TTG | 336 |
| Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu | |
| 100 105 110 | |
| GGA ATC TTG ACT AAG AGG TCA AAT TCC ACC CCA GCT ACC AAT GAG GCT | 384 |
| Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr Pro Ala Thr Asn Glu Ala | |
| 115 120 125 | |
| CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT GTG CTG CTG GGT CAG CCC | 432 |
| Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln Pro | |
| 130 135 140 | |
| AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC TTC CCT CCT GTG ATC AAC | 480 |
| Asn Thr Leu Ile Cys Phe Val Asn Ile Phe Pro Pro Val Ile Asn | |
| 145 150 155 160 | |
| ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC ACA GAC GGC GTT TAT GAG | 528 |
| Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr Glu | |
| 165 170 175 | |
| ACC AGC TTC CTT GTC AAC CGT GAC CAT TCC TTC CAC AAG CTG TCT TAT | 576 |
| Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser Tyr | |
| 180 185 190 | |
| CTC ACC TTC ATC CCT TCT GAC GAT GAT ATT TAT GAC TGC AAG GTG GAG | 624 |
| Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu | |
| 195 200 205 | |
| CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA CAC TGG GAA CCT GAG ATT | 672 |
| His Trp Gly Leu Glu Pro Val Leu Lys His Trp Glu Pro Glu Ile | |
| 210 215 220 | |
| CCA GCC CCC ATG TCA GAG CTG ACA GAG ACT | 702 |
| Pro Ala Pro Met Ser Glu Leu Thr Glu Thr | |
| 225 230 | |

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

| | |
|---|--|
| Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Gly Gly Gly | |
| 1 5 10 15 | |

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly
 20 25 30

Ser Gly Gly Gly Ser Glu Asp Asp Ile Glu Ala Asp His Val Gly
 35 40 45

Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr
 50 55 60

Thr His Glu Phe Asp Gly Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys
 65 70 75 80

Lys Glu Thr Ile Trp Met Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe
 85 90 95

Asp Pro Gln Gly Leu Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu
 100 105 110

Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr Pro Ala Thr Asn Glu Ala
 115 120 125

Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln Pro
 130 135 140

Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile Asn
 145 150 155 160

Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr Glu
 165 170 175

Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser Tyr
 180 185 190

Leu Thr Phe Ile Pro Ser Asp Asp Ile Tyr Asp Cys Lys Val Glu
 195 200 205

His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu Ile
 210 215 220

Pro Ala Pro Met Ser Glu Leu Thr Glu Thr
 225 230

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

| | |
|---|-----|
| GGG GAC ACC CGA CCA CGT TTC CTG TGG CAG CCT AAG AGG GAG TGT CAT | 48 |
| Gly Asp Thr Arg Pro Arg Phe Leu Trp Gln Pro Lys Arg Glu Cys His | |
| 1 5 10 15 | |
| TTC TTC AAT GGG ACG GAG CGG GTG CGG TTC CTG GAC AGA TAC TTC TAT | 96 |
| Phe Phe Asn Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr | |
| 20 25 30 | |
| AAC CAG GAG GAG TCC GTG CGC TTC GAC AGC GAC GTG GGG GAG TTC CGG | 144 |
| Asn Gln Glu Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg | |
| 35 40 45 | |
| GCG GTG ACG GAG CTG GGG CGG CCT GAC GCT GAG TAC TGG AAC AGC CAG | 192 |
| Ala Val Thr Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln | |
| 50 55 60 | |
| AAG GAC ATC CTG GAG CAG GCG CGG GCC GCG GTG GAC ACC TAC TGC AGA | 240 |
| Lys Asp Ile Leu Glu Gln Ala Arg Ala Val Asp Thr Tyr Cys Arg | |
| 65 70 75 80 | |
| CAC AAC TAC GGG GTT GTG GAG AGC TTC ACA GTG CAG CGG | 279 |
| His Asn Tyr Gly Val Val Glu Ser Phe Thr Val Gln Arg | |
| 85 90 | |

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

B30

| | |
|---|--|
| Gly Asp Thr Arg Pro Arg Phe Leu Trp Gln Pro Lys Arg Glu Cys His | |
| 1 5 10 15 | |
| Phe Phe Asn Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr | |
| 20 25 30 | |
| Asn Gln Glu Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg | |
| 35 40 45 | |
| Ala Val Thr Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln | |
| 50 55 60 | |
| Lys Asp Ile Leu Glu Gln Ala Arg Ala Val Asp Thr Tyr Cys Arg | |
| 65 70 75 80 | |
| His Asn Tyr Gly Val Val Glu Ser Phe Thr Val Gln Arg | |
| 85 90 | |

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: ZymoGenetics, Inc.
1201 Eastlake Avenue East
Seattle
WA
USA
98102

Sent B34

Anergen, Inc.
301 Penobscot Drive
Redwood City
CA
USA
94063

(ii) TITLE OF INVENTION: IMMUNE MEDIATORS AND RELATED METHODS

(iii) NUMBER OF SEQUENCES: 61

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: ZymoGenetics, Inc.
- (B) STREET: 1201 Eastlake Avenue East
- (C) CITY: Seattle
- (D) STATE: WA
- (E) COUNTRY: USA
- (F) ZIP: 98102

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/480,002
- (B) FILING DATE: 07-JUN-1995

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/483,241
- (B) FILING DATE: 07-JUN-1995

(viii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/482,133
- (B) FILING DATE: 07-JUN-1995

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 60/005,964
- (B) FILING DATE: 27-OCT-1995

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Parker, Gary E
- (B) REGISTRATION NUMBER: 31-648

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 206-442-6673
- (B) TELEFAX: 206-442-6678

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCGCAAGCTT GAATTGAGC TCATGGTG TG TCT

33

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

Sub
B³⁴

~~(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:~~

~~AATTCGATAT CATGGTGTGT CTGAAGCTCC CTGGAGGCTC CTGCATGACA GCGCTGAC~~

58

~~(2) INFORMATION FOR SEQ ID NO:3:~~

~~(i) SEQUENCE CHARACTERISTICS:~~

- ~~(A) LENGTH: 58 base pairs~~
- ~~(B) TYPE: nucleic acid~~
- ~~(C) STRANDEDNESS: single~~
- ~~(D) TOPOLOGY: linear~~

~~(ii) MOLECULE TYPE: cDNA~~

~~(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:~~

~~CACTGTCAGC GCTGTCATGC AGGAGCCTCC AGGGAGCTTC AGACACACCA TGATATCG~~

58

~~(2) INFORMATION FOR SEQ ID NO:4:~~

~~(i) SEQUENCE CHARACTERISTICS:~~

- ~~(A) LENGTH: 60 base pairs~~
- ~~(B) TYPE: nucleic acid~~
- ~~(C) STRANDEDNESS: single~~
- ~~(D) TOPOLOGY: linear~~

~~(ii) MOLECULE TYPE: cDNA.~~

~~(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:~~

~~ACTTCTTTAA AAACATCGTG ACTCCCGCGTA CACCCCCGCC ATCGGGAGGC GGGTCAGGTG~~

60

~~(2) INFORMATION FOR SEQ ID NO:5:~~

~~(i) SEQUENCE CHARACTERISTICS:~~

- ~~(A) LENGTH: 60 base pairs~~
- ~~(B) TYPE: nucleic acid~~
- ~~(C) STRANDEDNESS: single~~
- ~~(D) TOPOLOGY: linear~~

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATCCACCTG ACCCGCCTCC CGATGGCGGG GGTGTACGCG GAGTCACGAT GTTTTAAAG

60

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGTGACACTG ATGGTGCTGA GCTCCCCACT GGCTTGCT GACGAAAACC CAGTAGTGC

59

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGTGCACCA CTGGGTTTTC GTCAGACAAA GCCAGTGGGG AGCTCAGCAC CATCAGTGT

59

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCCGGCTGAT GCTCCCCGCT GCACTGT

27

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCGCTCTAGA TCATATAGTT GGAGC

25

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCAGGGTCTA GATCATAAAG GCCCTGGGTG TCTGGAG

37

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGAGGAATTC GCAGAGACCT CCCAGAGACC AGGATCC

37

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AACACTCTAG ATCACTGCAG GAGCCCTGCT GGAGGGAG

37

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGAGGAATTC TGAGTCCTGG TGACTGCCAT TACCTGT

37

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGAGGCATCAG CCGGCATCAA AGAAGAACAT

30

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAGGATGATT AAATGAGTCG CCTCTCGAAG GTGGCTCCAG TGATTAAGC CAGAATGATG

60

GAGTATGGAA CCACAGGAGG TGGAGGCTCT GGAGGTGGAG GCTCAGGAGG A

111

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGAGGCTCAG GAGGAGGTGG GTCCGGAGAC TCCGAAAGG

39

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGCGGGATCC GATCGTGGAG GATGATTAAA TG

32

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCCACCTGAT CCACCCCGCA GGGAGGTGGG

30

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGTGGATCAG GTGGCGAAGA CGACATTGAG

30

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCGGAATTCT TAACTAGTAG CTGGGGTGAA

30

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCGGAATTCT TAACTAGTAG CTGGGGTGAA

30

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCCACCTGAT CCACCCCGCA GGGAGGTGTG

30

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CGCGGGATCC GATCGTGGAG GATGATTAAA TGTTCTTAA AACATCGTG ACTCCGCGTA

60

CACCCCCGCC AGGAGGTGGA GGCTCTGGAG GTGGAGGCTC AGGAGGA

107

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCGGAATTCT TACTTGCTCC GGGCAGACTC

30

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGAGGGCTAG GAGGAGGTGG GTCTGGCGGT GGAGGTTCCG GCGGAGGCAG TTCAGAAAGAC

60

GACATTGAGG CC

72

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGCGGAGGTG GCTCAGGCAG AGGTGGATCT GGAGGTGGAG GCTCACGGCT TGAACAGCCC

60

AAT

63

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

| | |
|---|----|
| TGAGCCTCCA CCTCCAGATC CACCTCCGCC TGAGCCACCT CCGCCAGTCT CTGTCAGCTC | 60 |
| TGA | 63 |

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

| | |
|--------------------------------------|----|
| CCGGAATTCT TAACTAGTCT CTGTCAGCTC TGA | 33 |
|--------------------------------------|----|

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Gly Ala Ser Ala Gly

1 5

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Gly Gly Ser Gly Gly
1 5

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Gly Gly Gly Ser Gly Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
1 5 10 15
Gly Gly Gly Ser Gly Gly Gly Ser
20 25

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro Arg
1 5 10 15
Thr Pro Pro Pro Ser
20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gly Gly Ser Gly Gly Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGAGGGCTCAG GAGGA

15

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Pro Gly Gly Ala Ile Ser Asn Met Tyr Ala Met
1 5 10

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Pro Gly Gly Ala Ile Ser Asn Met Tyr Ala Met Met Ile Ala Arg Phe
1 5 10 15

Lys Met Phe Pro
20

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Pro Gly Gly Ala Ile Ser Asn Met Tyr Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS

(B) LOCATION: 1..654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

| | |
|--|-----|
| AGT CGC CTC TCG AAG GTG GCT CCA GTG ATT AAA GCC AGA ATG ATG GAG Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu | 48 |
| 1 5 10 15 | |
| TAT GGA ACC ACA GGA GGT GGA GGC TCT GGA GGT GGA GGC TCA GGA GGA Tyr Gly Thr Thr Gly Gly Ser Gly Gly Gly Ser Gly Gly | 96 |
| 20 25 30 | |
| GGT GGG TCC GGA GAC TCC GAA AGG CAT TTC GTG CAC CAG TTC AAG GGC Gly Gly Ser Gly Asp Ser Glu Arg His Phe Val His Gln Phe Lys Gly | 144 |
| 35 40 45 | |
| GAG TGC TAC TTC ACC AAC GGG ACG CAG CGC ATA CGG CTC GTG ACC AGA Glu Cys Tyr Phe Thr Asn Gly Thr Gln Arg Ile Arg Leu Val Thr Arg | 192 |
| 50 55 60 | |
| TAC ATC TAC AAC CGG GAG GAG TAC CTG CGC TTC GAC AGC GAC GTG GGC Tyr Ile Tyr Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly | 240 |
| 65 70 75 80 | |
| GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CAC TCA GCC GAG TAC TAC Glu Tyr Arg Ala Val Thr Glu Leu Gly Arg His Ser Ala Glu Tyr Tyr | 288 |
| 85 90 95 | |
| AAT AAG CAG TAC CTG GAG CGA ACG CGG GCC GAG CTG GAC ACG GCG TGC Asn Lys Gln Tyr Leu Glu Arg Thr Arg Ala Glu Leu Asp Thr Ala Cys | 336 |
| 100 105 110 | |
| AGA CAC AAC TAC GAG GAG ACG GAG GTC CCC ACC TCC CTG CGG GGT GGA Arg His Asn Tyr Glu Glu Thr Glu Val Pro Thr Ser Leu Arg Gly Gly | 384 |
| 115 120 125 | |
| TCA GGT GGC GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC TTC TAT GGT Ser Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly | 432 |
| 130 135 140 | |
| ACA ACT GTT TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu | 480 |
| 145 150 155 160 | |

| | |
|--|-----|
| TTT GAT GGT GAT GAG TTG TTC TAT GTG GAC TTG GAT AAG AAG AAA ACT Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr | 528 |
| 165. 170 175 | |
| GTC TGG AGG CTT CCT GAG TTT GGC CAA TTG ATA CTC TTT GAG CCC CAA Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln | 576 |
| 180 185 190 | |
| GGT GGA CTG CAA AAC ATA GCT GCA GAA AAA CAC AAC TTG GGA ATC TTG Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu | 624 |
| 195 200 205 | |
| ACT AAG AGG TCA AAT TTC ACC CCA GCT ACT Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr | 654 |
| 210 215 | |

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

| | |
|--|----|
| GGA GAC TCC GAA AGG CAT TTC GTG CAC CAG TTC AAG GGC GAG TGC TAC Gly Asp Ser Glu Arg His Phe Val His Gln Phe Lys Gly Glu Cys Tyr | 48 |
| 1 5 10 15 | |

| | |
|--|----|
| TTC ACC AAC GGG ACG CAG CGC ATA CGG CTC GTG ACC AGA TAC ATC TAC Phe Thr Asn Gly Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr | 96 |
| 20 25 30 | |

| | |
|--|-----|
| AAC CGG GAG GAG TAC CTG CGC TTC GAC AGC GAC GTG GGC GAG TAC CGC Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg | 144 |
| 35 40 45 | |

| | |
|--|-----|
| GCG GTG ACC GAG CTG GGG CGG CAC TCA GCC GAG TAC TAC AAT AAG CAG Ala Val Thr Glu Leu Gly Arg His Ser Ala Glu Tyr Tyr Asn Lys Gln | 192 |
| 50 55 60 | |
| TAC CTG GAG CGA ACG CGG GCC GAG CTG GAC ACG GCG TGC AGA CAC AAC Tyr Leu Glu Arg Thr Arg Ala Glu Leu Asp Thr Ala Cys Arg His Asn | 240 |
| 65 70 75 80 | |
| TAC GAG GAG ACG GAG GTC CCC ACC TCC CTG CGG Tyr Glu Glu Thr Glu Val Pro Thr Ser Leu Arg | 273 |
| 85 90 | |

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

| | |
|--|-----|
| GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val | 48 |
| 1 5 10 15 | |
| TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly | 96 |
| 20 25 30 | |
| GAT GAG TTG TTC TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg | 144 |
| 35 40 45 | |
| CTT CCT GAG TTT GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu | 192 |
| 50 55 60 | |

CAA AAC ATA GCT GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG
 Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg
 65 70 75 80

240

TCA AAT TTC ACC CCA GCT ACT
 Ser Asn Phe Thr Pro Ala Thr
 85

261

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs.
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TTC TTT AAA AAC ATC GTG ACT CCG CGT ACA CCC CCG CCA GGA GGT GGA
 Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Gly Gly Gly
 1 5 10 15

48

GGC TCT GGA GGT GGA GGC TCA GGA GGA GGT GGG TCC GGA GAC TCC GAA
 Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Asp Ser Glu
 20 25 30

96

AGG CAT TTC GTG TTC CAG TTC AAG GGC GAG TGC TAC TTC ACC AAC GGG
 Arg His Phe Val Phe Gln Phe Lys Gly Glu Cys Tyr Phe Thr Asn Gly
 35 40 45

144

ACG CAG CGC ATA CGA TCT GTG GAC AGA TAC ATC TAC AAC CGG GAG GAG
 Thr Gln Arg Ile Arg Ser Val Asp Arg Tyr Ile Tyr Asn Arg Glu Glu
 50 55 60

192

| | |
|---|-----|
| TAC CTG CGC TTC GAC AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu 65 70 75 80 | 240 |
| CTG GGG CGG CCA GAC CCC GAG TAC TAC AAT AAG CAG TAC CTG GAG CAA Leu Gly Arg Pro Asp Pro Glu Tyr Tyr Asn Lys Gln Tyr Leu Glu Gln 85 90 95 | 288 |
| ACG CGG GCC GAG CTG GAC ACG GTG TGC AGA CAC AAC TAC GAG GGG GTG Thr Arg Ala Glu Leu Asp Thr Val Cys Arg His Asn Tyr Glu Gly Val 100 105 110 | 336 |
| GAG ACC CAC ACC TCC CTG CGG GGT GGA TCA GGT GGC GAA GAC GAC ATT Glu Thr His Thr Ser Leu Arg Gly Gly Ser Gly Gly Glu Asp Asp Ile 115 120 125 | 384 |
| GAG GCC GAC CAC GTA GGC GTC TAT GGT ACA ACT GTA TAT CAG TCT CCT Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro 130 135 140 | 432 |
| GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TGG TTC Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Trp Phe 145 150 155 160 | 480 |
| TAT GTG GAC TTG GAT AAG AAG GAG ACT ATC TGG ATG CTT CCT GAG TTT Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met Leu Pro Glu Phe 165 170 175 | 528 |
| GGC CAA TTG ACA AGC TTT GAC CCC CAA GGT GGA CTG CAA AAC ATA GCT Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala 180 185 190 | 576 |
| ACA GGA AAA TAC ACC TTG GGA ATC TTG ACT AAG AGG TCA AAT TCC ACC Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr 195 200 205 | 624 |
| CCA GCT ACT Pro Ala Thr 210 | 633 |

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

| | |
|--|-----|
| GGA GAC TCC GAA AGG CAT TTC GTG TTC CAG TTC AAG GGC GAG TGC TAC Gly Asp Ser Glu Arg His Phe Val Phe Gln Phe Lys Gly Glu Cys Tyr | 48 |
| 1 5 10 15 | |
| TTC ACC AAC GGG ACG CAG CGC ATA CGA TCT GTG GAC AGA TAC ATC TAC Phe Thr Asn Gly Thr Gln Arg Ile Arg Ser Val Asp Arg Tyr Ile Tyr | 96 |
| 20 25 30 | |
| AAC CGG GAG GAG TAC CTG CGC TTC GAC AGC GAC GTG GGC GAG TAC CGC Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg | 144 |
| 35 40 45 | |
| GCG GTG ACC GAG CTG GGG CGG CCA GAC CCC GAG TAC TAC AAT AAG CAG Ala Val Thr Glu Leu Gly Arg Pro Asp Pro Glu Tyr Tyr Asn Lys Gln | 192 |
| 50 55 60 | |
| TAC CTG GAG CAA ACG CGG GCC GAG CTG GAC ACG GTG TGC AGA CAC AAC Tyr Leu Glu Gln Thr Arg Ala Glu Leu Asp Thr Val Cys Arg His Asn | 240 |
| 65 70 75 80 | |
| TAC GAG GGG GTG GAG ACC CAC ACC TCC CTG CGG Tyr Glu Gly Val Glu Thr His Thr Ser Leu Arg | 273 |
| 85 90 | |

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

| | |
|---|-----|
| GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC GTC TAT GGT ACA ACT GTA | 48 |
| Glu Asp Asp Ile Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val | |
| 1 5 10 15 | |
| TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT | 96 |
| Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly | |
| 20 25 30 | |
| GAT GAG TGG TTC TAT GTG GAC TTG GAT AAG AAG GAG ACT ATC TGG ATG | 144 |
| Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met | |
| 35 40 45 | |
| CTT CCT GAG TTT GGC CAA TTG ACA AGC TTT GAC CCC CAA GGT GGA CTG | 192 |
| Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu | |
| 50 55 60 | |
| CAA AAC ATA GCT ACA GGA AAA TAC ACC TTG GGA ATC TTG ACT AAG AGG | 240 |
| Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg | |
| 65 70 75 80 | |
| TCA AAT TCC ACC CCA GCT ACT | 261 |
| Ser Asn Ser Thr Pro Ala Thr | |
| 85 | |

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CATCGTGGAG GATGAT

16

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GAC GAA AAC CCA GTA GTG CAC TTC TTT AAA AAC ATC GTG ACT CCG CGT
 Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro Arg
 1 5 10 15

48

ACA CCC CCG CCA TCG GGA GGC GGG TCA GGT GGA TCC GGG GAC ACC CGA
 Thr Pro Pro Pro Ser Gly Gly Ser Gly Gly Ser Gly Asp Thr Arg
 20 25 30

96

CCA CGT TTC CTG TGG CAG CCT AAG AGG GAG TGT CAT TTC TTC AAT GGG
 Pro Arg Phe Leu Trp Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly
 35 40 45

144

ACG GAG CGG GTG CGG TTC CTG GAC AGA TAC TTC TAT AAC CAG GAG GAG
 Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu
 50 55 60

192

TCC GTG CGC TTC GAC AGC GAC GTG GGG GAG TTC CGG GCG GTG ACG GAG
 Ser Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu

240

| 65 | 70 | 75 | 80 | |
|--|-----|----|-----|-----|
| CTG GGG CGG CCT GAC GCT GAG TAC TGG AAC AGC CAG AAG GAC ATC CTG Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu | | | | 288 |
| 85 | 90 | | 95 | |
| GAG CAG GCG CGG GCC GCG GTG GAC ACC TAC TGC AGA CAC AAC TAC GGG Glu Gln Ala Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly | | | | 336 |
| 100 | 105 | | 110 | |
| GTT GTG GAG AGC TTC ACA GTG CAG CGG GGA GCA TCA GCC GGC ATC AAA Val Val Glu Ser Phe Thr Val Gln Arg Gly Ala Ser Ala Gly Ile Lys | | | | 384 |
| 115 | 120 | | 125 | |
| GAA GAA CAT GTG ATC ATC CAG GCC GAG TTC TAT CTG AAT CCT GAC CAA Glu Glu His Val Ile Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln | | | | 432 |
| 130 | 135 | | 140 | |
| TCA GGC GAA TTT ATG TTT GAC TTT GAT GGT GAT GAG ATT TTC CAT GTG Ser Gly Glu Phe Met Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val | | | | 480 |
| 145 | 150 | | 155 | 160 |
| GAT ATG GCA AAG AAG GAG ACG GTC TGG CGG CTT GAA GAA TTT GGA CGA Asp Met Ala Lys Lys Glu Thr Val Trp Arg Leu Glu Phe Gly Arg | | | | 528 |
| 165 | 170 | | 175 | |
| TTT GCC AGC TTT GAG GCT CAA GGT GCA TTG GCC AAC ATA GCT GTG GAC Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp | | | | 576 |
| 180 | 185 | | 190 | |
| AAA GCC AAC CTG GAA ATC ATG ACA AAG CGC TCC AAC TAT ATG ATC Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Met Ile | | | | 621 |
| 195 | 200 | | 205 | |

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GGG GAC ACC CGA CCA CGT TTC CTG TGG CAG CCT AAG AGG GAG TGT CAT
Gly Asp Thr Arg Pro Arg Phe Leu Trp Gln Pro Lys Arg Glu Cys His
1 5 10 15

48

TTC TTC AAT GGG ACG GAG CGG GTG CGG TTC CTG GAC AGA TAC TTC TAT
 Phe Phe Asn Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr
 20 25 30

96

AAC CAG GAG GAG TCC GTG CGC TTC GAC AGC .GAC GTG GGG GAG TTC CGG
Asn Gln Glu Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg
35 40 45

144

GCG GTG ACG GAG CTG GGG CGG CCT GAC GCT GAG TAC TGG AAC AGC CAG
 Ala Val Thr Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln
 50 55 60

192

AAG GAC ATC CTG GAG CAG CGG GCC GCG GTG GAC ACC TAC TGC AGA
 Lys Asp Ile Leu Glu Gln Ala Arg Ala Ala Val Asp Thr Tyr Cys Arg
 65 70 75 80

240

CAC AAC TAC GGG GTT GTG GAG AGC TTC ACA GTG CAG CGG
His Asn Tyr Gly Val Val Glu Ser Phe Thr Val Gln Arg
85 90

279

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

| | |
|--|-----|
| ATC AAA GAA GAA CAT GTG ATC ATC CAG GCC GAG TTC TAT CTG AAT CCT Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu Phe Tyr Leu Asn Pro | 48 |
| 1 5 10 15 | |
| GAC CAA TCA GGC GAA TTT ATG TTT GAC TTT GAT GGT GAT GAG ATT TTC Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp Gly Asp Glu Ile Phe | 96 |
| 20 25 30 | |
| CAT GTG GAT ATG GCA AAG AAG GAG ACG GTC TGG CGG CTT GAA GAA TTT His Val Asp Met Ala Lys Lys Glu Thr Val Trp Arg Leu Glu Glu Phe | 144 |
| 35 40 45 | |
| GGA CGA TTT GCC AGC TTT GAG GCT CAA GGT GCA TTG GCC AAC ATA GCT Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala | 192 |
| 50 55 60 | |
| GTG GAC AAA GCC AAC CTG GAA ATC ATG ACA AAG CGC TCC AAC TAT ATG Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Met | 240 |
| 65 70 75 80 | |
| ATC | 243 |
| Ile | |

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

| | |
|--|-----|
| TTC TTT AAA AAC ATC GTG ACT CCG CGT ACA CCC CCG CCA GGA GGT GGA Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Gly Gly Gly | 48 |
| 1 5 10 15 | |
| GGC TCT GGA GGT GGA GGC TCA GGA GGA GGT GGG TCT GGC GGT GGA GGT Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Gly | 96 |
| 20 25 30 | |
| TCC GGC GGA GGC GGT TCA GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC Ser Gly Gly Ser Glu Asp Asp Ile Glu Ala Asp His Val Gly | 144 |
| 35 40 45 | |
| GTC TAT GGT ACA ACT GTA TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr | 192 |
| 50 55 60 | |
| ACA CAT GAA TTT GAT GGT GAT GAG TGG TTC TAT GTG GAC TTG GAT AAG Thr His Glu Phe Asp Gly Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys | 240 |
| 65 70 75 80 | |
| AAG GAG ACT ATC TGG ATG CTT CCT GAG TTT GGC CAA TTG ACA AGC TTT Lys Glu Thr Ile Trp Met Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe | 288 |
| 85 90 95 | |
| GAC CCC CAA GGT GGA CTG CAA AAC ATA GCT ACA GGA AAA TAC ACC TTG Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu | 336 |
| 100 105 110 | |
| GGA ATC TTG ACT AAG AGG TCA AAT TCC ACC CCA GCT ACC AAT GAG GCT Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr Pro Ala Thr Asn Glu Ala | 384 |
| 115 120 125 | |
| CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT GTG CTG CTG GGT CAG CCC Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln Pro | 432 |
| 130 135 140 | |
| AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC TTC CCT CCT GTG ATC AAC Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile Asn | 480 |
| 145 150 155 160 | |
| ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC ACA GAC GGC GTT TAT GAG | 528 |

| | | | |
|---|-----|-----|-----|
| Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr Glu | | | |
| 165 | 170 | 175 | |
| ACC AGC TTC CTT GTC AAC CGT GAC CAT TCC TTC CAC AAG CTG TCT TAT | | | 576 |
| Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser Tyr | | | |
| 180 | 185 | 190 | |
| CTC ACC TTC ATC CCT TCT GAC GAT ATT TAT GAC TGC AAG GTG GAG | | | 624 |
| Leu Thr Phe Ile Pro Ser Asp Asp Ile Tyr Asp Cys Lys Val Glu | | | |
| 195 | 200 | 205 | |
| CAC TGG GGC CTG GAG CCG GTT CTG AAA CAC TGG GAA CCT GAG ATT | | | 672 |
| His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu Ile | | | |
| 210 | 215 | 220 | |
| CCA GCC CCC ATG TCA GAG CTG ACA GAG ACT | | | 702 |
| Pro Ala Pro Met Ser Glu Leu Thr Glu Thr | | | |
| 225 | 230 | | |

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 588 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

| | | | |
|---|---|----|----|
| GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC GTC TAT GGT ACA ACT GTA | | | 48 |
| Glu Asp Asp Ile Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val | | | |
| 1 | 5 | 10 | 15 |

| | | | |
|---|----|----|----|
| TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT | | | 96 |
| Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly | | | |
| 20 | 25 | 30 | |

| | | | | |
|--|-----|-----|-----|-----|
| GAT GAG TGG TTC TAT GTG GAC TTG GAT AAG AAG GAG ACT ATC TGG ATG Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met | 35 | 40 | 45 | 144 |
| CTT CCT GAG TTT GGC CAA TTG ACA AGC TTT GAC CCC CAA GGT GGA CTG Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu | 50 | 55 | 60 | 192 |
| CAA AAC ATA GCT ACA GGA AAA TAC ACC TTG GGA ATC TTG ACT AAG AGG Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg | 65 | 70 | 75 | 240 |
| TCA AAT TCC ACC CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC Ser Asn Ser Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe | 85 | 90 | 95 | 288 |
| CCC AAG TCC CCT GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe | 100 | 105 | 110 | 336 |
| GTG GAC AAC ATC TTC CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT Val Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn | 115 | 120 | 125 | 384 |
| AGC AAG TCA GTC ACA GAC GGC GTT TAT GAG ACC AGC TTC CTT GTC AAC Ser Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn | 130 | 135 | 140 | 432 |
| CGT GAC CAT TCC TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT Arg Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser | 145 | 150 | 155 | 160 |
| GAC GAT GAT ATT TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu | 165 | 170 | 175 | 528 |
| CCG GTT CTG AAA CAC TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG Pro Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu | 180 | 185 | 190 | 576 |
| CTG ACA GAG ACT Leu Thr Glu Thr | | | | 588 |
| | 195 | | | |

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TTC TTT AAA AAC ATC GTG ACT CCG CGT ACA CCC CCG CCA GGA GGT GGA
 Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Gly Gly Gly
 1 5 10 15

48

GGC TCT GGA GGT GGA GGC TCA GGA GGA GGT GGG TCC GGA GAC TCC GAA
 Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Asp Ser Glu
 20 25 30

96

AGG CAT TTC GTG TTC CAG TTC AAG GGC GAG TGC TAC TTC ACC AAC GGG
 Arg His Phe Val Phe Gln Phe Lys Gly Glu Cys Tyr Phe Thr Asn Gly
 35 40 45

144

ACG CAG CGC ATA CGA TCT GTG GAC AGA TAC ATC TAC AAC CGG GAG GAG
 Thr Gln Arg Ile Arg Ser Val Asp Arg Tyr Ile Tyr Asn Arg Glu Glu
 50 55 60

192

TAC CTG CGC TTC GAC AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG
 Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu
 65 70 75 80

240

CTG GGG CGG CCA GAC CCC GAG TAC TAC AAT AAG CAG TAC CTG GAG CAA
 Leu Gly Arg Pro Asp Pro Glu Tyr Tyr Asn Lys Gln Tyr Leu Glu Gln
 85 90 95

288

ACG CGG GCC GAG CTG GAC ACG GTG TGC AGA CAC AAC TAC GAG GGG GTG
 Thr Arg Ala Glu Leu Asp Thr Val Cys Arg His Asn Tyr Glu Gly Val

336

| | | | |
|--|-----|-----|-----|
| 100 | 105 | 110 | |
| GAG ACC CAC ACC TCC CTG CGG GGT GGA TCA GGT GGC GAA GAC GAC ATT Glu Thr His Thr Ser Leu Arg Gly-Gly Ser Gly Glu Asp Asp Ile | | | 384 |
| 115 | 120 | 125 | |
| GAG GCC GAC CAC GTA GGC GTC TAT GGT ACA ACT GTA TAT CAG TCT CCT Glu Ala Asp His Val Gly Val Tyr Thr Thr Val Tyr Gln Ser Pro | | | 432 |
| 130 | 135 | 140 | |
| GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TGG TTC Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Trp Phe | | | 480 |
| 145 | 150 | 155 | 160 |
| TAT GTG GAC TTG GAT AAG AAG GAG ACT ATC TGG ATG CTT CCT GAG TTT Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met Leu Pro Glu Phe | | | 528 |
| 165 | 170 | 175 | |
| GGC CAA TTG ACA AGC TTT GAC CCC CAA GGT GGA CTG CAA AAC ATA GCT Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala | | | 576 |
| 180 | 185 | 190 | |
| ACA GGA AAA TAC ACC TTG GGA ATC TTG ACT AAG AGG TCA AAT TCC ACC Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr | | | 624 |
| 195 | 200 | 205 | |
| CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTG CCC AAG TCC CCT Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro | | | 672 |
| 210 | 215 | 220 | |
| GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val Asn Ile | | | 720 |
| 225 | 230 | 235 | 240 |
| TTC CCT CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val | | | 768 |
| 245 | 250 | 255 | |
| ACA GAC GGC GTT TAT GAG ACC AGC TTC CTT GTC AAC CGT GAC CAT TCC Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser | | | 816 |
| 260 | 265 | 270 | |
| TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAC GAT GAT ATT Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Ile | | | 864 |
| 275 | 280 | 285 | |

| | |
|---|------|
| TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys 290 295 300 | 912 |
| CAT TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG CTG ACA GAG ACT His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr 305 310 315 320 | 960 |
| GGC GGA GGT GGC TCA GGC GGA GGT GGA TCT GGA GGT GGA GGC TCA CGG Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Arg 325 330 335 | 1008 |
| CTT GAA CAG CCC AAT GTC GTC ATC TCC CTG TCC AGG ACA GAG GCC CTC Leu Glu Gln Pro Asn Val Val Ile Ser Leu Ser Arg Thr Glu Ala Leu 340 345 350 | 1056 |
| AAC CAC CAC AAC ACT CTG GTC TGC TCA GTG ACA GAT TTC TAC CCA GCC Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro Ala 355 360 365 | 1104 |
| AAG ATC AAA GTG CGC TGG TTC CGG AAT GGC CAG GAG GAG ACG GTG GGG Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr Val Gly 370 375 380 | 1152 |
| GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC TGG ACC TTC CAG GTC Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln Val 385 390 395 400 | 1200 |
| CTG GTC ATG CTG GAG ATG ACC CCT CGG CGG GGA GAG GTC TAC ACC TGC Leu Val Met Leu Glu Met Thr Pro Arg Arg Gly Glu Val Tyr Thr Cys 405 410 415 | 1248 |
| CAC GTG GAG CAT CCG AGC CTG AAG AGC CCC ATC ACT GTG GAG TGG AGG His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp Arg 420 425 430 | 1296 |
| GCA CAG TCT GAG TCT GCC CGG AGC AAG Ala Gln Ser Glu Ser Ala Arg Ser Lys 435 440 | 1323 |

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CGG CTT GAA CAG CCC AAT GTC GTC ATC TCC CTG TCC AGG ACA GAG GCC
 Arg Leu Glu Gln Pro Asn Val Val Ile Ser Leu Ser Arg Thr Glu Ala
 1 5 10 15

48

CTC AAC CAC AAC ACT CTG GTC TGC TCA GTG ACA GAT TTC TAC CCA
 Leu Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro
 20 25 30

96

GCC AAG ATC AAA GTG CGC TGG TTC CGG AAT GGC CAG GAG GAG ACG GTG
 Ala Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Thr Val
 35 40 45

144

GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC TGG ACC TTC CAG
 Gly Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln
 50 55 60

192

GTC CTG GTC ATG CTG GAG ATG ACC CCT CGG CGG GGA GAG GTC TAC ACC
 Val Leu Val Met Leu Glu Met Thr Pro Arg Arg Gly Glu Val Tyr Thr
 65 70 75 80

240

TGC CAC GTG GAG CAT CCG AGC CTG AAG AGC CCC ATC ACT GTG GAG TGG
 Cys His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp
 85 90 95

288

AGG GCA CAG TCT GAG TCT GCC CGG AGC AAG
 Arg Ala Gln Ser Glu Ser Ala Arg Ser Lys
 100 105

318

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

AGT CGC CTC TCG AAG GTG GCT CCA GTG ATT AAA GCC AGA ATG ATG GAG
 Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu
 1 5 10 15

48

TAT GGA ACC ACA GGA GGT GGA GGC TCT GGA GGT GGA GGC TCA GGA GGA
 Tyr Gly Thr Thr Gly Gly Ser Gly Gly Gly Ser Gly Gly 20 25 30

96

GGT GGG TCC GGA GAC TCC GAA AGG CAT TTC GTG CAC CAG TTC AAG GGC
 Gly Gly Ser Gly Asp Ser Glu Arg His Phe Val His Gln Phe Lys Gly
 35 40 45

144

GAG TGC TAC TTC ACC AAC GGG ACG CAG CGC ATA CGG CTC GTG ACC AGA
 Glu Cys Tyr Phe Thr Asn Gly Thr Gln Arg Ile Arg Leu Val Thr Arg
 50 55 60

192

TAC ATC TAC AAC CGG GAG GAG TAC CTG CGC TTC GAC AGC GAC GTG GGC
 Tyr Ile Tyr Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly
 65 70 75 80

240

| | |
|---|-----|
| GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CAC TCA GCC GAG TAC TAC Glu Tyr Arg Ala Val Thr Glu Leu Gly Arg His Ser Ala Glu Tyr Tyr 85 90 95 | 288 |
| AAT AAG CAG TAC CTG GAG CGA ACG CGG GCC GAG CTG GAC ACG GCG TGC Asn Lys Gln Tyr Leu Glu Arg Thr Arg Ala Glu Leu Asp Thr Ala Cys 100 105 110 | 336 |
| AGA CAC AAC TAC GAG GAG ACG GAG GTC CCC ACC TCC CTG CGG GGT GGA Arg His Asn Tyr Glu Glu Thr Glu Val Pro Thr Ser Leu Arg Gly Gly 115 120 125 | 384 |
| TCA GGT GGC GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC TTC TAT GGT Ser Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly 130 135 140 | 432 |
| ACA ACT GTT TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu 145 150 155 160 | 480 |
| TTT GAT GGT GAT GAG TTG TTC TAT GTG GAC TTG GAT AAG AAG AAA ACT Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Thr 165 170 175 | 528 |
| GTC TGG AGG CTT CCT GAG TTT GGC CAA TTG ATA CTC TTT GAG CCC CAA Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln 180 185 190 | 576 |
| GGT GGA CTG CAA AAC ATA GCT GCA GAA AAA CAC AAC TTG GGA ATC TTG Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu 195 200 205 | 624 |
| ACT AAG AGG TCA AAT TTC ACC CCA GCT ACC AAT GAG GCT CCT CAA GCG Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala 210 215 220 | 672 |
| ACT GTG TTC CCC AAG TCC CCT GTG CTG CTG GGT CAG CCC AAC ACC CTT Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu 225 230 235 240 | 720 |
| ATC TGC TTT GTG GAC AAC ATC TTC CCA CCT GTG ATC AAC ATC ACA TGG Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp 245 250 255 | 768 |
| CTC AGA AAT AGC AAG TCA GTC ACA GAC GGC GTT TAT GAG ACC AGC TTC | 816 |

| | | | | |
|---|-----|-----|-----|------|
| Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe | | | | |
| 260 | 265 | 270 | | |
| CTC GTC AAC CGT GAC CAT TCC TTC CAC AAG CTG TCT TAT CTC ACC TTC | | | | 864 |
| Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe | | | | |
| 275 | 280 | 285 | | |
| ATC CCT TCT GAT GAT GAC ATT TAT GAC TGC AAG GTG GAG CAC TGG GGC | | | | 912 |
| Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly | | | | |
| 290 | 295 | 300 | | |
| CTG GAG GAG CCG GTT CTG AAA CAC TGG GAA CCT GAG ATT CCA GCC CCC | | | | 960 |
| Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro | | | | |
| 305 | 310 | 315 | 320 | |
| ATG TCA GAG CTG ACA GAG ACT GGC GGA GGT GGC TCA GGC GGA GGT GGA | | | | 1008 |
| Met Ser Glu Leu Thr Glu Thr Gly Gly Ser Gly Gly Gly Gly Gly | | | | |
| 325 | 330 | 335 | | |
| TCT GGA GGT GGA GGC TCA CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC | | | | 1056 |
| Ser Gly Gly Ser Arg Leu Glu Glu Pro Asn Val Ala Ile Ser | | | | |
| 340 | 345 | 350 | | |
| CTG TCC AGG ACA GAG GCC CTC AAC CAC AAC ACT CTG GTC TGT TCG | | | | 1104 |
| Leu Ser Arg Thr Glu Ala Leu Asn His His Asn Thr Leu Val Cys Ser | | | | |
| 355 | 360 | 365 | | |
| GTG ACA GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT | | | | 1152 |
| Val Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg Trp Phe Arg Asn | | | | |
| 370 | 375 | 380 | | |
| GGC CAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT | | | | 1200 |
| Gly Glu Glu Thr Val Gly Val Ser Ser Thr Glu Leu Ile Arg Asn | | | | |
| 385 | 390 | 395 | 400 | |
| GGG GAC TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT | | | | 1248 |
| Gly Asp Trp Thr Phe Glu Val Leu Val Met Leu Glu Met Thr Pro His | | | | |
| 405 | 410 | 415 | | |
| CAG GGA GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC | | | | 1296 |
| Gln Gly Glu Val Tyr Thr Cys His Val Glu His Pro Ser Leu Lys Ser | | | | |
| 420 | 425 | 430 | | |

CCC ATC ACT GTG GAG TGG AGG GCA CAG TCC GAG TCT GCC CGG AGC AAG 1341
 Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser Ala Arg Ser Lys
 435 440 445

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT 48
 Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val
 1 5 10 15

TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT 96
 Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly
 20 25 30

GAT GAG TTG TTC TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG 144
 Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg
 35 40 45

CTT CCT GAG TTT GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG 192
 Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu
 50 55 60

CAA AAC ATA GCT GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG 240
 Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg
 65 70 75 80

| | | | | |
|--|-----|-----|-----|-----|
| TCA AAT TTC ACC CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC Ser Asn Phe Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe | 85 | 90 | 95 | 288 |
| CCC AAG TCC CCT GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe | 100 | 105 | 110 | 336 |
| GTG GAC AAC ATC TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT Val Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn | 115 | 120 | 125 | 384 |
| AGC AAG TCA GTC ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC Ser Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn | 130 | 135 | 140 | 432 |
| CGT GAC CAT TCC TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT Arg Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser | 145 | 150 | 155 | 480 |
| GAT GAT GAC ATT TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu | 165 | 170 | 175 | 528 |
| CCG GTT CTG AAA CAC TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG Pro Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu | 180 | 185 | 190 | 576 |
| CTG ACA GAG ACT Leu Thr Glu Thr | 195 | | | 588 |

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

| | |
|---|-----|
| CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC AGG ACA GAG GCC | 48 |
| Arg Leu Glu Gln Pro Asn Val Ala Ile Ser Leu Ser Arg Thr Glu Ala | |
| 1 5 10 15 | |
| CTC AAC CAC AAC ACT CTG GTC TGT TCG GTG ACA GAT TTC TAC CCA | 96 |
| Leu Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro | |
| 20 25 30 | |
| GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG GAG GAG ACA GTG | 144 |
| Ala Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr Val | |
| 35 40 45 | |
| GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC TGG ACC TTC CAG | 192 |
| Gly Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln | |
| 50 55 60 | |
| GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA GAG GTC TAC ACC | 240 |
| Val Leu Val Met Leu Glu Met Thr Pro His Gln Gly Glu Val Tyr Thr | |
| 65 70 75 80 | |
| TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC ACT GTG GAG TGG | 288 |
| Cys His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp | |
| 85 90 95 | |
| AGG GCA CAG TCC GAG TCT GCC CGG | 312 |
| Arg Ala Gln Ser Glu Ser Ala Arg | |
| 100 105 | |

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu
1 5 10 15
Tyr Gly Thr Thr
20

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Lys Pro Lys Ala Thr Ala Glu Gln Leu Lys Thr Val Met Asp Asp
1 5 10 15